NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure
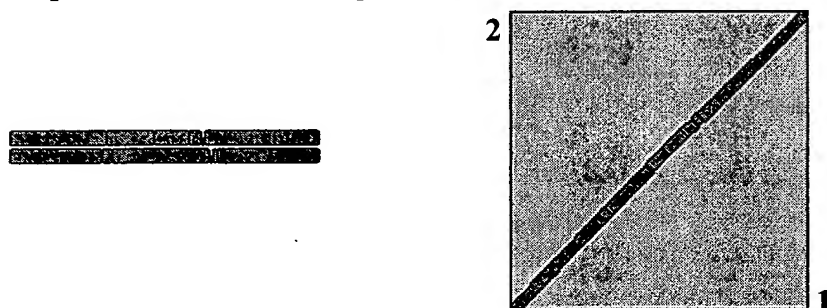
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Align

Sequence 1 lcl|seq_1 **Length** 862 (1 .. 862)

Sequence 2 lcl|seq_2 **Length** 859 (1 .. 859)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 1202 bits (3110), Expect = 0.0
Identities = 637/869 (73%), Positives = 704/869 (80%), Gaps = 17/869 (1%)
```

```
Query: 1    MERAESSSTEPAKAIKPIDRKSVHQICSGQVVLSLSTAVKELVENSLDAGATNIDLKLKD 60
            ME+ E  STE AKAIKPID KSVHQICSGQV+LSLSTAVKEL+ENS+DAGAT IDL+LKD
Sbjct: 1    MEQTEGVSTECAKAIKPIDGKSVHQICSGQVILSLSTAVKELIENSVDAGATTIDLRLKD 60

Query: 61   YGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120
            YGVDLIEVSDNGCGVEEENFEGL LKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV
Sbjct: 61   YGVDLIEVSDNGCGVEEENFEGLALKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120

Query: 121  TISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQRNIKKE 180
            TISTCH SA VGTRL+FDHNGKI QKTPYPRP+GTTVSVQ LF TLPVR+KEFQRNIKKE
Sbjct: 121  TISTCHGSASVGTRLVFDHNGKITQKTPYPRPKGTTVSVQHLFYTLPVRYKEFQRNIKKE 180

Query: 181  YAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSIKENIGSVFGQKQLQSLI 240
            Y+KMVQVL AYCIISAG+RVSCTNQLGQGKR  VVCT G+  +KENIGSVFGQKQLQSLI
Sbjct: 181  YSKMVQVLQAYCIISAGVRVSCTNQLGQGKRHAVVCTSGTSGMKENIGSVFGQKQLQSLI 240

Query: 241  PFVQLPPSDSVCEEYGLSCSDALHNLF--YISGFISQCTHGVGRSSTDRQFFFINRRPCD 298
            PFVQLPPSD+VCEEYGLS S   H F ++ F S T  G   T   F   R P
Sbjct: 241  PFVQLPPSDAVCEEYGLSTSGR-HKTFSTFRASFHSARTAPGGVQQTG-SFSSSIRGPVT 298

Query: 299  PAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358
             +   L     YHMYNRHQYPFVVLN+SVDSECVDINVTPDKRQILLQEEKLLLAVLKTS
Sbjct: 299  QQRSLSLSMRFYHMYNRHQYPFVVLNVSVDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358

Query: 359  LIGMFDSDVNKLNVSQQPLLDVEGNLIKMHAADLEKPMVEKQDQSPSLR-TGEEKKDVSI 417
            LIGMFDSD NKLNV+QQPLLDVEGNL+K+H A+LEKP+ KQD SPSL+ T +EK+  SI
```

```
Sbjct:  359  LIGMFDSDANKLNVNQQPLLDVEGNLVKLHTAELEKPVPGKQDNSPSLKSTADEKRVASI  418

Query:  418  SRLREAFSLRHTTENKPHSPKTPEPRRSPLGQKRGMLSSSTSGAISDKGVLRPQKEAVSS  477
             SRLREAFSL   T E K    P+T E  RS    +KRG+LSS  S   IS +G+   Q + VS
Sbjct:  419  SRLREAFSLHPTKEIKSRGPETAELTRSFPSEKRGVLSSYPSDVISYRGLRGSQDKLVSP  478

Query:  478  SHGPSDPTDRAEVEKDSGHGSTSVDSEG-FSIPDTGSHCSSEYAASSPGDRGSQEHVDSQ  536
             +  P D  DR ++EKDSG  STS  SE  FS P+  S  SS+Y  SS  DR SQE ++
Sbjct:  479  TDSPGDCMDREKIEKDSGLSSTSAGSEEEFSTPEVASSFSSDYNVSSLEDRPSQETINCG  538

Query:  537  E---KAPETDDSFSDVDCHSNQEDTGCKFRVLPQPTNLATPNTKRFKKEEILSSSDICQK  593
             +    + P T S        ED G + + LP    L+  N KRFK  EE  S+ +I Q+
Sbjct:  539  DLDCRPPGTGQSLKP-------EDHGYQCKALPL-ARLSPTNAKRFKTEERPSNVNISQR  590

Query:  594  LVNTQDMSASQVDVAVKINKKVVPLDFSMSSLAKRIKQLHHEAQQSEGEQNYRKFRAKIC  653
             L   Q   SA++VDVA+K NK++V L+FS+SSLAKR+KQL H    Q++ E +YRKFRAKIC
Sbjct:  591  LPGPQSTSAAEVDVAIKMNKRIVLLEFSLSSLAKRMKQLQHLKAQNKHELSYRKFRAKIC  650

Query:  654  PGENQAAEDELRKEISKTMFAEMEIIGQFNLGFIITKLNEDIFIVDQHATDEKYNFEMLQ  713
             PGENQAAEDELRKEISK+MFAEMEI+GQFNLGFI+TKL ED+F+VDQHA DEKYNFEMLQ
Sbjct:  651  PGENQAAEDELRKEISKSMFAEMEILGQFNLGFIVTKLKEDLFLVDQHAADEKYNFEMLQ  710

Query:  714  QHTVLQGQRLIAPQTLNLTAVNEAVLIENLEIFRKNGFDFVIDENAPVTERAKLISLPTS  773
             QHTVLQ QRLI PQTLNLTAVNEAVLIENLEIFRKNGFDFVIDE+APVTERAKLISLPTS
Sbjct:  711  QHTVLQAQRLITPQTLNLTAVNEAVLIENLEIFRKNGFDFVIDEDAPVTERAKLISLPTS  770

Query:  774  KNWTFGPQDVDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMIGTALNTSEMKKLITH  833
             KNWTFGPQD+DELIFMLSDSPGVMCRPSRV+QMFASRACRKSVMIGTALN SEMKKLITH
Sbjct:  771  KNWTFGPQDIDELIFMLSDSPGVMCRPSRVRQMFASRACRKSVMIGTALNASEMKKLITH  830

Query:  834  MGEMDHPWNCPHGRPTMRHIANLGVISQN  862
             MGEMDHPWNCPHGRPTMRH+ANL VISQN
Sbjct:  831  MGEMDHPWNCPHGRPTMRHVANLDVISQN  859
```

CPU time: 0.17 user secs.   0.04 sys. secs   0.21 total secs.

```
Lambda     K       H
  0.315    0.131    0.371
```

Gapped
```
Lambda     K       H
  0.267    0.0410   0.140
```

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 6158
Number of Sequences: 0
Number of extensions: 502
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 859
length of database: 461,760,005
effective HSP length: 136
effective length of query: 723
effective length of database: 461,759,869

effective search space: 333852385287
effective search space used: 333852385287
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 79 (35.0 bits)